

## SEQUENCE LISTING

<110> William Gaarde  
Susan M. Freier  
Andrew T. Watt

<120> ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION

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**PATENT**

-31-

**RTS-0189**

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Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile	
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<210> 58

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<400> 58

taggctcaat gatatcactg

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<210> 59

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<211> 20

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<400> 67

caggaagaga gctggtcaat

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<210> 68

<211> 20

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<400> 68

acaggaagag agctggtcaa

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<210> 69

<211> 20

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<400> 69

tcctgttcta tgctgctggt

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<210> 70

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<210> 71

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<210> 76

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<210> 78

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<400> 79

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<400> 82

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<210> 83

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<210> 84

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<400> 84

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<210> 85

<211> 20

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<400> 85

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<210> 86

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<210> 87

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<210> 88

<211> 20

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<223> Antisense Oligonucleotide

<400> 88

ggacactaga ggctgtgcag

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<210> 89

<211> 20

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<223> Antisense Oligonucleotide

<400> 89

gccctgctct gaggtgagcg

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<210> 90

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<210> 91

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<210> 92

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<210> 93

<211> 20

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<210> 94

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<400> 94

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<210> 95

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tcgtcagtct gtgtacacta

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<210> 97

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Met Glu Gln Pro Gln Glu Glu Thr Pro Glu Ala Arg Glu Glu Glu Lys  
1 5 10 15

gag gaa gtg gcc atg ggt gac gga gcc ccg gag ctc aat ggg gga cca 153  
Glu Glu Val Ala Met Gly Asp Gly Ala Pro Glu Leu Asn Gly Gly Pro  
20 25 30

gaa cac acg ctt cct tcc agc agc tgt gca gac ctc tcc cag aat tcc 201  
Glu His Thr Leu Pro Ser Ser Ser Cys Ala Asp Leu Ser Gln Asn Ser  
35 40 45

tcc cct tcc tcc ctg ctg gac cag ctg cag atg ggc tgt gat ggg gcc 249  
Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala  
50 55 60

tca ggc ggc agc ctc aac atg gaa tgt cgg gtg tgc ggg gac aag gcc 297  
Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala  
65 70 75 80

tcg ggc ttc cac tac ggg gtc cac gcg tgc gag ggg tgc aag ggc ttc 345  
Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe  
85 90 95

ttc cgc cgg aca atc cgc atg aag ctc gag tat gag aag tgc gat cgg 393  
Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg  
100 105 110

atc tgc aag atc cag aag aag aac cgc aac aag tgt cag tac tgc cgc 441  
Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg  
115 120 125

ttc cag aag tgc ctg gca ctc ggc atg tcg cac aac gct atc cgc ttt 489  
Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe

130	135	140	
gga cgg atg ccg gag gcc gag aag agg aag ctg gtg gcg ggg ctg act			537
Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu Thr			
145	150	155	160
gcc agc gag ggg tgc cag cac aac ccc cag ctg gcc gac ctg aag gcc			585
Ala Ser Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala			
	165	170	175
ttc tct aag cac atc tac aac gcc tac ctg aaa aac ttc aac atg acc			633
Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr			
	180	185	190
aaa aag aag gcc cgg agc atc ctc acc ggc aag tcc agc cac aac gca			681
Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala			
	195	200	205
ccc ttt gtc atc cac gac atc gag aca ctg tgg cag gca gag aag ggc			729
Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly			
	210	215	220
ctg gtg tgg aaa cag ctg gtg aac ggg ctg ccg ccc tac aac gag atc			777
Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile			
	225	230	235
agt gtg cac gtg ttc tac cgc tgc cag tcc acc aca gtg gag aca gtc			825
Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val			
	245	250	255
cga gag ctc acc gag ttc gcc aag aac atc ccc aac ttc agc agc ctc			873
Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu			
	260	265	270
ttc ctc aat gac cag gtg acc ctc ctc aag tat ggc gtg cac gag gcc			921
Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala			
	275	280	285
atc ttt gcc atg ctg gcc tcc atc gtc aac aaa gac ggg ctg ctg gtg			969

Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val	
290	300
gcc aac ggc agt ggc ttc gtc acc cac gag ttc ttg cga agt ctc cgc	1017
Ala Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg	
305	320
aag ccc ttc agt gac atc att gag ccc aag ttc gag ttt gct gtc aag	1065
Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys	
325	335
ttc aat gcg ctg gag ctc gat gac agt gac ctg gcg ctc ttc atc gcg	1113
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala	
340	350
gcc atc att ctg tgt gga gac cgg cca ggc ctc atg aat gtg ccc cag	1161
Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln	
355	365
gta gaa gcc atc cag gac acc att ctg cgg gct cta gaa ttc cat ctg	1209
Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu	
370	380
cag gtc aac cac cct gac agc cag tac ctc ttc ccc aag ctg ctg cag	1257
Gln Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln	
385	400
aag atg gca gac ctg cgg cag ctg gtc act gag cat gcc cag atg atg	1305
Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met Met	
405	415
cag tgg cta aag aag acg gag agt gag acc ttg ctg cac ccc ctg ctc	1353
Gln Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu Leu His Pro Leu Leu	
420	430
cag gaa atc tac aag gac atg tac taa ggccgcagcc caggcctccc	1400
Gln Glu Ile Tyr Lys Asp Met Tyr	
435	440

ctcaggctct gctgggcca gccacggact gttcagagga ccagccacag gcactggcag 1460  
tcaagcagct agagcctact cacaacactc cagacacgtg gccagactc tcccccaaca 1520  
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<212> DNA

<213> M. musculus

<220>

<400> 98

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ctcctgctca ctgacagatg aagacaaacc cacggtaaag gcagtccatc tgcgctcaga 180  
cccagatggg ggcagagcta tgaccaggcc tgcaggcgcc acgccaagtg ggggtcagtc 240  
atggaacagc cacaggagga gaccctgag gcccggaag aggagaaaga ggaagtggcc 300  
atgggtgacg gagccccgga gctcaatggg ggacaaaaac aaacaaacaa acaagcaaac 360  
aaaaaaacta cagtcaaaat ctaatttgaa aaatatttct gcctttatta ttacttattt 420  
gattttgggc cctgggagaa tggactgagg tacataattt acattgcaaa gcagaccag 480  
ggacg 485

<210> 99

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<212> DNA

<213> M. musculus

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<222> (1)...(1323)

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Glu Glu Val Ala Met Gly Asp Gly Ala Pro Glu Leu Asn Gly Gly Pro				
20 25 30				
gaa cac acg ctt cct tcc agc agc tgt gca gac ctc tcc cag aat tcc				144
Glu His Thr Leu Pro Ser Ser Ser Cys Ala Asp Leu Ser Gln Asn Ser				
35 40 45				
tcc cct tcc tcc ctg ctg gac cag ctg cag atg ggc tgt gat ggg gcc				192
Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala				
50 55 60				
tca ggc ggc agc ctc aac atg gaa tgt cgg gtg tgc ggg gac aag gcc				240
Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala				
65 70 75 80				
tcg ggc ttc cac tac ggg gtc cac gcg tgc gag ggg tgc aag ggc ttc				288
Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe				
85 90 95				
ttc cgc cgg aca atc cgc atg aag ctc gag tat gag aag tgc gat cgg				336
Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg				
100 105 110				
atc tgc aag atc cag aag aag aac cgc aac aag tgt cag tac tgc cgc				384
Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg				
115 120 125				
ttc cag aag tgc ctg gca ctc ggc atg tcg cac aac gct atc cgc ttt				432
Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe				
130 135 140				
gga cgg atg ccg gac ggc gag aag agg aag ctg gtg gcg ggg ctg act				480
Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr				
145 150 155 160				
gcc agc gag ggg tgc cag cac aac ccc cag ctg gcc gac ctg aag gcc				528

Ala Ser Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala	
165 170 175	
ttc tct aag cac atc tac aac gcc tac ctg aaa aac ttc aac atg acc	576
Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr	
180 185 190	
aaa aag aag gcc cgg agc atc ctc acc ggc aag tcc agc cac aac gca	624
Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala	
195 200 205	
ccc ttt gtc atc cac gac atc gag aca ctg tgg cag gca gag aag ggc	672
Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly	
210 215 220	
ctg gtg tgg aaa cag ctg gtg aac ggg ctg ccg ccc tac aac gag atc	720
Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile	
225 230 235 240	
agt gtg cac gtg ttc tac cgc tgc cag tcc acc aca gtg gag aca gtc	768
Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val	
245 250 255	
cga gag ctc acc gag ttc gcc aag aac atc ccc aac ttc agc agc ctc	816
Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu	
260 265 270	
ttc ctc aat gac cag gtg acc ctc ctc aag tat ggc gtg cac gag gcc	864
Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala	
275 280 285	
atc ttt gcc atg ctg gcc tcc atc gtc aac aaa gac ggg ctg ctg gtg	912
Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val	
290 295 300	
gcc aac ggc agt ggc ttc gtc acc cac gag ttc ttg cga agt ctc cgc	960
Ala Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg	
305 310 315 320	

aag ccc ttc agt gac atc att gag ccc aag ttc gag ttt gct gtc aag 1008  
 Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys  
                             325                            330                            335

ttc aat gcg ctg gag ctc gat gac agt gac ctg gcg ctc ttc atc gcg 1056  
 Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala  
                             340                            345                            350

gcc atc att ctg tgt gga gac cgg cca ggc ctc atg aat gtg ccc cag 1104  
 Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln  
                             355                            360                            365

gta gaa gcc atc cag gac acc att ctg cgg gct cta gaa ttc cat ctg 1152  
 Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu  
                             370                            375                            380

cag gtc aac cac cct gac agc cag tac ctc ttc ccc aag ctg ctg cag 1200  
 Gln Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln  
                             385                            390                            395                            400

aag atg gca gac ctg cgg cag ctg gtc act gag cat gcc cag atg atg 1248  
 cag tgg cta aag aag acg gag agt gag acc ttg ctg cac ccc ctg ctc 1296  
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gttgtagta ggctctagct

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<210> 107

<211> 20

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<400> 107

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**RTS-0189**

**-141-**

**PATENT**

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**RTS-0189**

**-142-**

**PATENT**

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**RTS-0189**

**-144-**

**PATENT**

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**RTS-0189**

**-153-**

**PATENT**

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**RTS-0189**

**-155-**

**PATENT**

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RTS-0189

-162-

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**RTS-0189**

**-163-**

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**-175-**

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